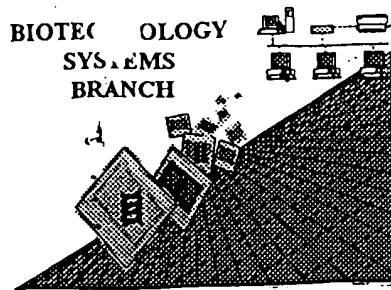


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0590

1109

*June*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/978423

Source: OIPE

Date Processed by STIC: 11/2/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION
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SERIAL NUMBER: 09/978,423

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 \_\_\_\_\_ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 \_\_\_\_\_ Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 \_\_\_\_\_ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 \_\_\_\_\_ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 \_\_\_\_\_ PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 \_\_\_\_\_ Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 \_\_\_\_\_ Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 \_\_\_\_\_ Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) 157 missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 \_\_\_\_\_ PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 11/02/2001

PATENT APPLICATION: US/09/978,423

TIME: 15:15:06

Input Set : A:\Seq\_Listing\_for\_P2630P1C21.wpd

Output Set: N:\CRF3\11022001\I978423.raw

Does Not Comply  
Corrected Diskette Needed

Errors on p. 4 & error pp. 1+2

3 <110> APPLICANT: Ashkenazi, Avi  
4 Baker Kevin P.  
5 Botstein, David  
6 Desnoyers, Luc  
7 Eaton, Dan  
8 Ferrara, Napoleon  
9 Filvaroff, Ellen  
10 Fong, Sherman  
11 Gao, Wei-Qiang  
12 Gerber, Hanspeter  
13 Gerritsen, Mary E.  
14 Goddard, Audrey  
15 Godowski, Paul J.  
16 Grimaldi, J. Christopher  
17 Gurney, Austin L.  
18 Hillan, Kenneth J  
19 Kljavin, Ivar J.  
20 Kuo, Sophia S.  
21 Napier, Mary A.  
22 Pan, James;  
23 Paoni, Nicholas F.  
24 Roy, Margaret Ann  
25 Shelton, David L.  
26 Stewart, Timothy A.  
27 Tumas, Daniel  
28 Williams, P. Mickey  
29 Wood, William I.  
31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
32 Acids Encoding the Same  
34 <130> FILE REFERENCE: P2630P1C21  
C--> 36 <140> CURRENT APPLICATION NUMBER: US/09/978,423  
C--> 36 <141> CURRENT FILING DATE: 2001-10-16  
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37 <151> PRIOR FILING DATE: 2001-07-30  
39 <150> PRIOR APPLICATION NUMBER: 60/062250  
40 <151> PRIOR FILING DATE: 1997-10-17  
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43 <151> PRIOR FILING DATE: 1997-11-03  
45 <150> PRIOR APPLICATION NUMBER: 60/065311  
46 <151> PRIOR FILING DATE: 1997-11-13  
48 <150> PRIOR APPLICATION NUMBER: 60/066364  
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52 <151> PRIOR FILING DATE: 1998-03-10  
54 <150> PRIOR APPLICATION NUMBER: 60/077632  
55 <151> PRIOR FILING DATE: 1998-03-11  
57 <150> PRIOR APPLICATION NUMBER: 60/077641

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/978,423

DATE: 11/02/2001

TIME: 15:15:06

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Output Set: N:\CRF3\11022001\I978423.raw

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## RAW SEQUENCE LISTING

DATE: 11/02/2001

PATENT APPLICATION: US/09/978,423

TIME: 15:15:06

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Output Set: N:\CRF3\11022001\I978423.raw

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## RAW SEQUENCE LISTING

DATE: 11/02/2001

PATENT APPLICATION: US/09/978,423

TIME: 15:15:06

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Output Set: N:\CRF3\11022001\I978423.raw

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should be 1998-05-07; some <sup>error</sup> on lines  
870+445

## RAW SEQUENCE LISTING

DATE: 11/02/2001

PATENT APPLICATION: US/09/978,423

TIME: 15:15:06

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Output Set: N:\CRF3\11022001\I978423.raw

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349 <151> PRIOR FILING DATE: 1999-05-14  
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,423

DATE: 11/02/2001

TIME: 15:15:07

Input Set : A:\Seq\_Listing\_for\_P2630P1C21.wpd

Output Set: N:\CRF3\11022001\I978423.raw

L:36 M:270 C: Current Application Number differs, Replaced Current Application No  
L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:244 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:370 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:445 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
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L:1043 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:1045 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:1552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
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L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
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L:3386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
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L:6223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152  
L:6225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,423

DATE: 11/02/2001

TIME: 15:15:07

Input Set : A:\Seq\_Listing\_for\_P2630P1C21.wpd

Output Set: N:\CRF3\11022001\I978423.raw

L:6387 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:157  
L:6389 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:6389 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:7713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191  
L:7719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191  
L:7729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191  
L:8724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215  
L:10653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265  
L:10655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265  
L:10657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265

09/978,423

Error P. 1

ctgttggcct ctggggctgt catggccac gcgttttgca aagtttgtga 1350  
ctcaccattc aaggccccga gtcttgact gtgaagcatc tgccatggg 1400  
aagtgtgtt tgttatcctt tctctgtggc agtgaagaag gaagaaatga 1450  
gagtctagac tcaagggaca ctggatggca agaattgtgc tgatgggtga 1500  
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<210> 157

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Error P.2

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 157

→ Must give explanation. See error summary sheet Item 11.

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
1				5					10					15

Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
				245					250					255

Ile	Arg	Glu	Gln	Gln	Arg	Ser	Ala	Val	Ser	Thr	Ser	Trp	Leu	Leu
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